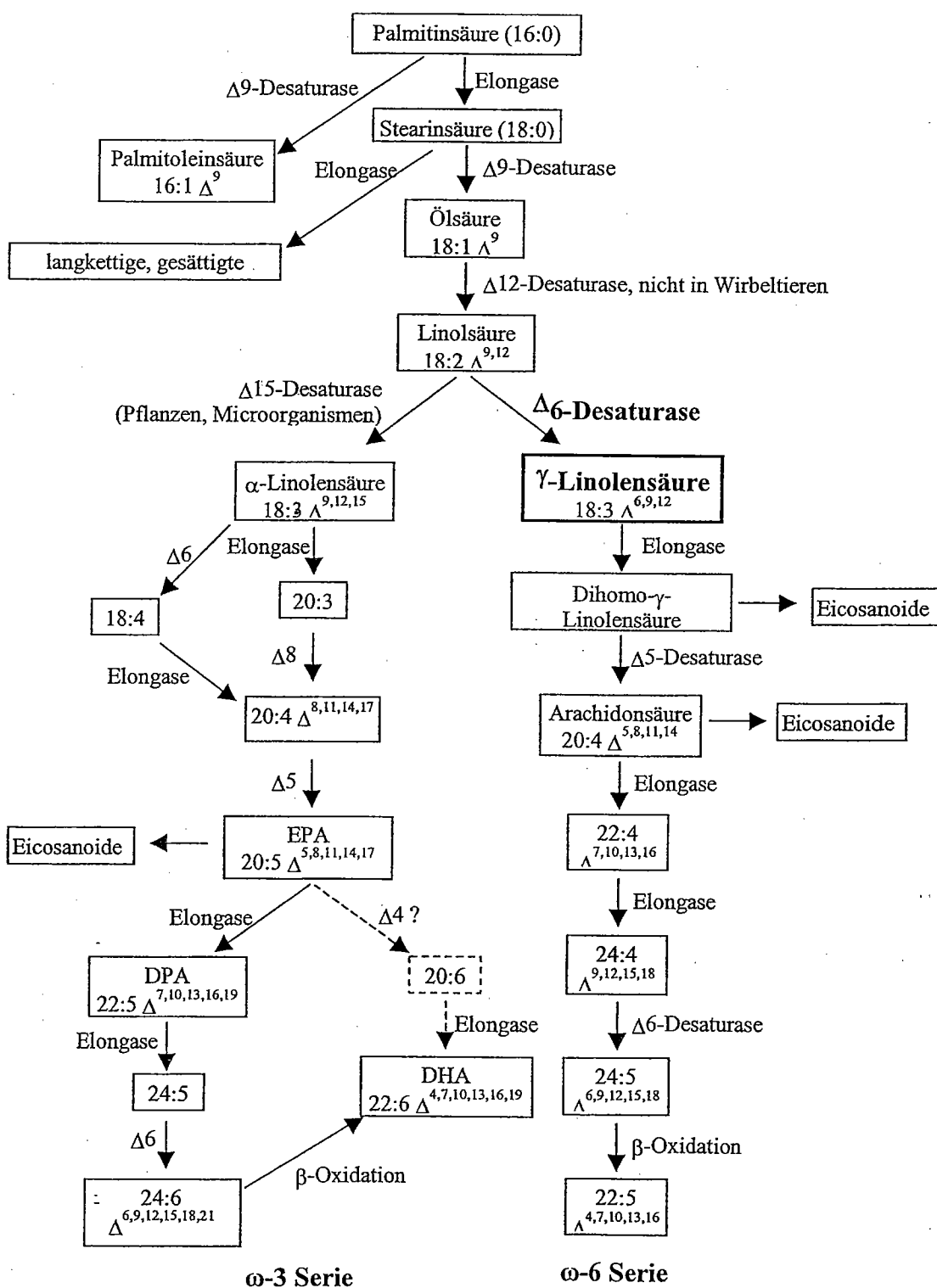


Figure 1



## Figure 2

BLASTP 2.0.8 [Jan-05-1999]

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Query= T.thermophila, delta-6-Desaturase (352 letters)

Database: /LION/data/db/fast/nrdb

387,705 sequences; 119,829,732 total letters

Sequences producing significant alignments:		Score (bits)	E Value
trembl AF078796 AF078796_1 gene: "des-5"; product: "delta 5 fat...		79	4e-14
trembl AF031477 AF031477_1 product: "delta6-fatty-acid-desatura...		79	4e-14
trembl Z81122 CET13F2_1 gene: "T13F2.1"; Caenorhabditis elegan...		78	1e-13
trembl Z70271 CEW08D2_2 gene: "W08D2.4"; Caenorhabditis elegan...		78	1e-13
trembl AF005096 AF005096_1 product: "desaturase/cytochrome b5 p...		70	3e-11
trembl AJ222980 PPAJ2980_1 gene: "des6"; product: "delta6-acyl-...		69	6e-11
trembl U79010 BOU79010_1 product: "delta 6 desaturase"; Borago...		67	2e-10
trembl AC005397 AC005397_14 gene: "T3F17.14"; product: "putativ...		67	2e-10
trembl AF007561 AF007561_1 product: "delta-6-Desaturase"; Bora...		66	4e-10
tremblnew AF126799 AF126799_1 product: "delta-6 fatty acid desa...		64	2e-09
tremblnew AF126798 AF126798_1 product: "delta-6 fatty acid desa...		63	3e-09
trembl AF031194 AF031194_1 gene: "S276"; product: "S276"; Trit...		62	6e-09
tremblnew AB021980 AB021980_1 product: "delta-6 fatty acid desa...		62	6e-09
tremblnew AL078610 SCH35_12 gene: "SCH35.42c"; product: "putati...		62	8e-09
trembl AJ224160 BNAJ4160_1 gene: "sld1"; product: "delta-8 sphi...		60	2e-08
trembl AC004770 AC004770_2 product: "BC269730_2"; Homo sapiens...		60	3e-08
trembl AJ224161 ATAJ4161_1 gene: "sld1"; product: "delta-8 sphi...		59	6e-08
tremblnew AL050118 HSM800210_1 gene: "DKFZp586C201"; product: "...		57	2e-07
trembl AB022097 AB022097_1 product: "delta 5 fatty acid desatur...		57	2e-07
trembl X87143 HACYTB5RN_1 product: "cytochrome b5 containing fu...		50	2e-05
trembl Y08460 MMMDES_1 gene: "Mdes"; product: "Mdes protein"; ...		50	3e-05
trembl AF001394 AF001394_1 product: "fatty acid desaturase/cyto...		46	4e-04
trembl AF002668 HSAF2668_1 product: "MLD"; Homo sapiens putati...		46	5e-04
swiss Q08871 LLCD_SYNY3 LINOLEOYL-COA DESATURASE (EC 1.14.99.25...		43	0.003

### Figure 3A

>aageneseq|W95504|W95504 Mortierella alpina delta 6 desaturase. Length = 457

Score = 89.7 bits (219), Expect = 4e-18

Identities = 102/422 (24%), Positives = 152/422 (35%), Gaps = 88/422 (20%)

```

Query: 9  EIVLENKPELLNEYKFIYKDEYDCTEYAKSNKHPGGNLNLFIDEKQDLTEYFRTLHS 68
      E + E K +      + I + YD E+      HPGG L      +D T+ F T H
Sbjct: 19  EALNEGKKDAEAPFLMIIDNKVYDVREFVPD--HPGGSVILT---HVGKDGTDVFDTFHP 73

Query: 69  KQALKILKSFPKGTGAKQEETE-SSKRFSILKKLKLHLEPNWPIEIG----LFLTTFTLF 123
      + A + L +F      + + + + F+      +KL+ LF+      +      F +F L
Sbjct: 74  EAAWETLANFYVGDIDESDRDIKNDFAAEVRKLRTLQSLGYYDSSKAYYAFKVSEFNL 133

Query: 124  VTGCLT---QKW-----YFSIPLLVLMQIISGWIGHSMNHNRPILR---KFALVY 168
      + G T      KW      S LL L      GW+ H      H++      R      F
Sbjct: 134  IWGLSTVIVAKWGQTSTLANVLSAALLGLFWQQCGWLAHDFLHHQVFQDRFWGDLFGAPL 193

Query: 169  APLCGGFSNKWWGRKHNQHMMFTNNILKDEDIQ-HDYKLWQ----- 208
      +C GFS+ WW KHN HH N +D DI H W
Sbjct: 194  GGVCQGFSSSWWKDKHNTTHHAAPNVHGEPDIDTHPLLTWSEHALEMFSVDPDEELTRMW 253

Query: 209  -----FP---FLFLKWKLDSIL-----ASYEFEGIFLALHWV 238
      FP F L W L SIL      E + LA+HW
Sbjct: 254  SRFMVLNQTFYFPILSFARLSWCLQSILFVLPNGQAHKPSGARVPISLVEQLSLAMHWT 313

Query: 239  LLFNQNFYIV-----ILSELIAGFFSASILVGNHEN--EMKFERRITLPFFEHI 286
      F +      ++S+ + G A + NH      + E + + FF QI
Sbjct: 314  WYLATMFLFIKDPVNMLVYFLVSQAVCGNLLAIVFSLNHNMGMPVISKEEAVIDMDFFTKQI 373

Query: 287  AASRNYAFHDIFSLIMGGMQYQTEHHFFPQIPFYRLPKARVIIAEELKKWNLKIHEGPI 346
      R+      +F+      GG+ YQ EHH FP +P + K + +      KK+N++ H +
Sbjct: 374  ITGRD-VHPGLFANWFTGGLNYQIEHHLFSPMPRHNFSKIQPAVETLCKKYNVRYHTTGM 432

Query: 347  FE 348
      E
Sbjct: 433  IE 434

```

### Figure 3B

>trembl|AF031477|AF031477\_1 product: "delta6-fatty-acid-desaturase";  
 Caenorhabditis elegans delta6-fatty-acid-desaturase mRNA, complete cds.  
 //:gp|AF031477|3088520 product: "delta6-fatty-acid-desaturase";  
 Caenorhabditis elegans delta6-fatty-acid-desaturase mRNA, complete cds.  
 Length = 443

Score = 79.2 bits (192), Expect = 4e-14

Identities = 100/390 (25%), Positives = 132/390 (33%), Gaps = 95/390 (24%)

Query: 41 KHPGGLNFLNLFIDEKQDLTEYFRTLH--SKQALKILKSFPKTGAKQE--ETESSKR--- 93  
 KHPGG D T F H S QA K L K G E E + KR  
 Sbjct: 28 KHPGGAIVIEQY---RNSDATHIFHAFHEGSSQAYKQLDLLKKHGEHDEFLEKQLEKRLDK 84

Query: 94 -----FSILKKKLKH--LFEPNWPIEIGLFLTTFTLFVTGCLTQ 130  
 F L++KL L + N + ++T ++ Q  
 Sbjct: 85 VDINVSAYDVSVAQEKKMVESFEKLRQKLHDDGLMKANETYFLFKAISTLSIMAFAYLQ 144

Query: 131 K--WYF-SIPLLVLMQIISGWIGHSMNHNHNR---NPILRKFAIVYAPLCGGFSNKWWGRK 183  
 WY S LL L GW+ H H + P+ +L + GFS WW K  
 Sbjct: 145 YLGWYITSACLLALAWQQFGWLTHEFCHQQPTKNRPLNDTISLFFGNFLQGFSRDWWKDK 204

Query: 184 HNQHMMFTNNILKDEDI-----QHDKLWQFPFLF 213  
 HN HH TN I D DI QH Y P L  
 Sbjct: 205 HNTTHAATNVIDHDGDIIDLAPLFAFIPGDLCKYKASF EKAILKIVPYQHLYFTAMLPLMR 264

Query: 214 LKWKLDLSILASYE-----FEGIFLALHWVLLFNQNFYI-----VILS 251  
 W S+ + E +E + HW +F Q F + I+S  
 Sbjct: 265 FSWTGQSVQWVFKENQMEYKVYQRNAFWEQATIVGHWAUVFYQLFLLPTWPLRVAYFIIS 324

Query: 252 ELIAGFFSASILVGNHENEMKF--ERRITLPFFEHQIAASRNYAFHDIFSLLIMGGMQYQ 309  
 ++ G A ++ NH + K+ RI F QI +RN L GG+ YQ  
 Sbjct: 325 QMGGGLLIAHVVTFNHNSVDKYPANSRILNNFAALQILTTRNMTPSPFIDWL-WGGLNYQ 383

Query: 310 TEHHFFPQIPFYRLPKARVIIAEELKKWNL 339  
 EHH FP +P L + E K+ NL  
 Sbjct: 384 IEHHLFPTMPCNLNACVKYVKEWCKENNL 413

### Figure 3C

>trembl|U79010|BOU79010\_1 product: "delta 6 desaturase"; Borago officinalis delta 6 desaturase mRNA, complete cds. //:gp|U79010|2062403 product: "delta 6 desaturase"; Borago officinalis delta 6 desaturase mRNA, complete cds. Length = 448

Score = 67.1 bits (161), Expect = 2e-10  
Identities = 100/414 (24%), Positives = 154/414 (37%), Gaps = 100/414 (24%)

```

Query: 6   TQEEIVLENKPELLNEYKFIYKDTEYDCTEYAKSNKHPGGLNFLNLFIDEKQDLTEYFRT 65
          T +E+  +KP  +      +   YD +++ K   HPGG  L      Q++T+ F
Sbjct: 10  TSDELKNHDKP---GDLWISIQGKAYDVSDWVKD--HPGGSFPLKSLAG--QEVTDAFVA 62

Query: 66  LHSKQALKILKSFPKTGAKQEE---TESSK-----RFSILKKKLKHLFEPNWPIE 112
          H      K L F  TG  ++  +E SK              +  +  KK  +F      I
Sbjct: 63  FHPASTWKNLDFK-FTGYLLKDYSEVSKDYRKLVFEFKMGFLYDKKGHIMFATLCFIA 121

Query: 113 IGLFLTTF-TLFVTGCLTQKWYFSIPLLVLMIISGWIGHSMNHN---NPILRKFAVY 168
          +  ++ +  LF  G L      FS  L+  + I SGWIGH  H      +  L KF  ++
Sbjct: 122 MLFAMSVYGVLFCEGVLVH--LFSGCLMGFLWISQGWIGHDAGHYMVVSDSRLNKFMGIF 179

Query: 169 APLC-GGFSNKWWGRKHNQHMMFTNNILKDEDIQH----- 202
          A  C  G S  WW      HN HH+  N++  D D+Q+
Sbjct: 180 AANCLSGISIGWWKWNHNAHHIACNSLEYDPDLQYIPFLVSSKFFGSLTSHFYEKRLTF 239

Query: 203 -----DYKLWQFPFLFLKWKLDASILASY-----YEFEGIFLALHWVLL- 240
          Y+ W F  +      +L+  + S              +E G  +  W  L
Sbjct: 240 DSLSRFFVSYQHWTTFYPIMCAARLNMYVQSLIMLLTKRNVSYRAHELLGCLVFSIWYPLL 299

Query: 241 -----FNQNFYIVILSELIAGF-----FSASILVGNHENEMKFERRITLPFFE HQ 285
          + +      VI S  + G              FS+S+ VG  +      FE++ T      +
Sbjct: 300 VSCLPNWGERIMFVIASLSVTGMQQVQFSLNHFSSSVYVGKPKGNNWFEKQ-TDGTLDIS 358

Query: 286 IAASRNYAFHDIFSLIMGGMQYQTEHHFFPQIPFYRLPKARVIIAEELKKWNL 339
          ++ FH      GG+Q+Q EHH FP++P  L K      + E  KK NL
Sbjct: 359 CPPWMDW-FH-----GGLQFQIEHHLFPKMPCNLRKISPYVIELCKKHNL 403

```

### Figure 3D

>tremblnew|AF126799|AF126799\_1 product: "delta-6 fatty acid desaturase";  
Homo sapiens delta-6 fatty acid desaturase mRNA, complete cds.  
//:gp|AF126799|4406528 product: "delta-6 fatty acid desaturase"; Homo  
sapiens delta-6 fatty acid desaturase mRNA, complete cds. Length = 444

Score = 63.6 bits (152), Expect = 2e-09

Identities = 92/390 (23%), Positives = 152/390 (38%), Gaps = 88/390 (22%)

```
Query: 31  YDCTEYAKSNKHPGGLNFLNLFIDEKQDLTEYFRTLHSKQAL--KILK-----SFPKTGA 83
          Y+ T++ S +HPGG  + + E D T+ FR H      K LK
Sbjct: 44  YNITKW--SIQHPGGQRVIGHYAGE--DATDAFRAFHPDLEFVGKFLKPLLIGELAPEEP 99

Query: 84  KQEETESSK---RFSILKKKLLK--HLFEPNWPPIEIGLF-----LTTFTLFVTGCLTQ 130
          Q+ ++SK   F L+K + +LF+ N      + L      + FT+F G
Sbjct: 100 SQDHGKNSKITEDFRALRKTAEDMNLFKTNHVFFLLLLAHIIIALESIAWFTVIFYFGNGWI 159

Query: 131 KWFYSIPLLVLMQIISGWIGHSMNH-----NRNPILRKFFALVYAPLCGGFSNKWWGRK 183
          + +L  Q  +GW+ H  H      N ++ KF + +      G S  WW  +
Sbjct: 160 PTLITAFVLATSQAQAGWLQHDYGHLSVYRKPKWNHLVHKFVIGHLK---GASANWWNHR 216

Query: 184 HNQHMHMTNNILKDEDIQ--HDYKL--WQFPFLFLKWKL-----DSIL 222
          H QHH  N   KD D+  H + L  WQ P  + K KL      ++
Sbjct: 217 HFQHHAKPNIFHKDPDVNMLHVFLGEWQ-PIEYGKKKLKYLPPYNHQHEYFFLIGPPLLI 275

Query: 223 ASYYEFEGI-----FLALHWVLLFNQNFYIV-----ILSELIAGFFSASILVGNH- 267
          Y++++ I      ++ L W + +  F+I      IL L+ F +  + +H
Sbjct: 276 PMYFQYQIIMTMIVHKNWVDLAWAVSYYIRFFITYIPFYGILGALL--FLNFIRFLESHW 333

Query: 268 -----ENEMKFERRITLPFFEHQIAASRNA---FHDIFSLLIMGGMQYQTEHHFFP 316
          M+ ++      +F  Q+ A+ N      F+D FS  G + +Q EHH FP
Sbjct: 334 FVWVTQMNHIVMEIDQEAYRDWFSSQLTATCNVEQSFFNDWFS----GHLNFQIEHHLFP 389

Query: 317 QIPFYRLPKARVIAEELKKWNLKIHEGP 346
          +P + L K  ++      K  ++  E P+
Sbjct: 390 TMPRHNHLHKIAPLVKSLCAKHGIEYQEKPL 419
```

### Figure 3E

>swiss|Q08871|LLCD\_SYNY3 LINOLEOYL-COA DESATURASE (EC 1.14.99.25)  
 (DELTA(6)-DESATURASE).//:treml|L11421|SSD6DS\_1 product: "delta-6-  
 Desaturase"; Synechocystis sp. delta-6-Desaturase gene, complete cds.  
 //:treml|D90914|SSD914\_112 gene: "des6"; product: "delta-6-Desaturase";  
 Synechocystis sp. PCC6803 complete genome, 16/27, 1991550-2137258.  
 //:pironly|S35157|S35157 Delta(6)-desaturase - Synechocystis  
 sp.//:gp|D90914|1653589 gene: "des6"; product: "delta-6-Desaturase";  
 Synechocystis sp. PCC6803 complete genome, 16/27, 1991550-2137258.  
 //:gp|L11421|349563 product: "delta-6-Desaturase"; Synechocystis sp. delta-  
 6-Desaturase gene, complete cds. Length = 359

Score = 43.4 bits (100), Expect = 0.003

Identities = 63/288 (21%), Positives = 101/288 (34%), Gaps = 61/288 (21%)

Query: 120 FTLFVTGCLTQKWYFSIPLLVLMQIISGWIGHSMNHNRR--NP-ILRKFALVYAPLCGGF 175  
 F LF + + L + + S +GH NHN NP I R + Y + G  
 Sbjct: 57 FVLFPVIFPVRLGCMVLAIALAASFNVGHDANHNAYSSNPHINRVLGMTYDFV--GL 114

Query: 176 SNKWWGRKHNQ-HHMFNTNNILKDEDIQHDYKLWQFPFL-----FLKWKLDASILAS 224  
 S+ W +HN HH +TN + D +I D + P F W L +  
 Sbjct: 115 SSFLWRYRHNYLHHTYTNI LGHDVEIHGDGAVRMSPEQEHVGIYRFQQFYIWLGLYLFIPF 174

Query: 225 YYEFEGIFLAL-----HWVLLFNQNFYIVILS-----ELIAGFFSASILVG 265  
 Y+ ++L L H + F +L L GF +L+G  
 Sbjct: 175 YWFLYDVYLVLNKGKYHDKIPPFQPLELASLLGIKLLWLGYVFGGLPLALGFSIPEVLIG 234

Query: 266 NHENEMKFERRI-TLPFFEHE-----QIAASRNYAFHDIFSL 300  
 M + + T+ H QI + N+A ++ F  
 Sbjct: 235 ASVTYMTYGIVVCTIFMLAHVLESTEFLLTPDGESGAIDDEWAICQIRTTANFATNNPFWN 294

Query: 301 LIMGGMQYQTEHHFFPQIPFYRLPKARVIIAEELKKWNLKIHEGPIFE 348  
 GG+ +Q HH FP I P+ II + +++ ++ P F+  
 Sbjct: 295 WFCGGLNHQVTHHLFPNICHIHYPQLENIIKDVCQEFQVEYKVYPTFK 342

Replacement Sheet  
Figure 4A

M.alpina 1 -----MAAAPSVRTFTTRAEVLNAEALNEGCKKDAEAPELMIIIDNKVYDVREHVP--DHPGG  
C.elegans 1 -----MVLREQE---HEPFFIKIDGKWCQIDDAVLR-SHPGG  
B.officinalis 1 -----MAAQIKKYITSDLEKNHDK---PGDLWISIQKAYDVSDWK--DHPGG  
M.musculus 1 MGKGGNQEGSTERQAPMPTFRWEEIQKHNLRTDRMLVLDKRVNVTKWSQ--RHPGG  
T.thermophila 1 -----MGVDKTQEEELVLENKPELLNEYKFIYKDTETEDCTEYAKSNKHHPGG

10  
M.alpina 54 -SVILLTHVCK--DGTDVFDTEHPEA---AWETLANFYVCGDIDESDRDIKND-----D--  
C.elegans 34 -SALTITMYKNM--DAITVFHHTFTGSKEAQWLTTELKKECPTQEPDIPDIKDDPIKGIDDV  
B.officinalis 45 SFPLKSLAQ--EVTDAFVAHPAS---TWKNLDKFFTGYYLKDYSVSEVS-----  
M.musculus 57 HRVIGHYSGE--DAIDAFRAFHLDLD--FVGKFLKPLLICELAPEEPEPSIDRG-----  
T.thermophila 46 LNFENLFIIDEKQDLTEYFRILHSKQ----ALKILKSFPKTGAKQEE--TESS-----

20  
M.alpina 100 -----FAAEVR-----KIRTLFQSLGYVDSSKAYAYAFKVSENLCTWGLSIVIVAKW  
C.elegans 91 NMGTFNISEKRSQAQINKSFTDLRMVRVRAEGLMDGSPLEFYIRKL-----LETFTITFFAFY  
B.officinalis 91 -----KDYR-----KLIVFEFSKMGLYD-KKGHIMFAT-LCFIAMLFAMSYYCVL  
M.musculus 105 -KSSQITTEDFR-----ALKKTAEDVNLKTNHLEFFLLSHIIVMESLAWFELSYF  
T.thermophila 92 -----KR-----FSILKKKIKHLFEPNWPPIEL-----GLFLTITFTTIFVT

25  
M.alpina 146 GQTSTLANVLISAALLGIMFMQCCGMLAHDFLHHQVFOQDRFWGDLFGAFLGVCQ-----  
C.elegans 146 LQYHTYY-LPSAILMGVAMQQLGMLIHEFAHHQLEFKNRYNDLEASYFVGNFLQVSHIFNN  
B.officinalis 133 FCEGVLVHLFSGCLMGFLMIQSGWIGHDACHYMMVSDSRINKFMGIFAANCLIS-----  
M.musculus 155 GTGWIP-TLVIAFVLATSQAQAGWLQHDYGHLSVYKKSIIWNHVVHKEVIGHLK-----  
T.thermophila 126 GCLTQKW-YFSIPLLVLMQIISGMIGHSMNHNRPILR----KFALVYAPLCG-----



# Replacement Sheet

Figure 4B

199 M.alpina GFSSNWKDKHNTTHAAPNVHGEDPDIDTHPLLTWSEHALEMFS--VPDEELTRMWSRF  
 205 C.elegans GFSSCGWKEQHNVHHAATNVVGRDGDLDLVPFYATVAEHLNNYS----QDS----WVMT  
 186 B.officinalis GISIGWKNWNAHHTACNSLEYDPDEQYHFFLVSSKFFGSLTSHFYEKRLTFDSLSRF  
 207 M.musculus GASANWNNHRHFQHHAKPNIFFKDPDIKSLHVFVLGEWQPLEYG----KKK----LKYL  
 174 T.thermophila GFSNKNWGRKHNQHMMFTNNILKDED-----I-----

257 M.alpina MVLNQTWEXFPILSEARLSWCLQSILFVLPNGQAHKPSGARVPISLVEQLSLAMHMTWYL  
 256 C.elegans LFRWQHVVHTFMLPELRLSWLLQSILFVSQMP-THYYDYRN-TAIYEQVGLSIHWAMSL  
 246 B.officinalis FVSYQHWTFFYPIMCAARLNMYVOSTIMLLTKR----NVSYRA----QELLGCLVFSIWNYP  
 258 M.musculus PYNHQHEYEFLIGPPLILPMYFQYQIIMFMIS-----RR-----DWVDLAWAISXYM  
 201 T.thermophila ----QHDYKLWQFPFLELKWKLDSILASYEF-----ECIFLALHMMVLLF

317 M.alpina ATMFLFLIKDPVNM--LVYFLVVSQAVCGNLLAIVFSINHGMPVISKEEAVDMDRFTKQII  
 314 C.elegans G-QLYFLPDWSTR--IMFFLVSHLVCGFLLSHVVTFNHYSVEKFASSNIMSNYACLIQIM  
 298 B.officinalis L-LVSCIPNNGER--LMFVIALSLVTG-MQQVQFSTNHFSSSVYVCK-PKGNMWFKEQTD  
 305 M.musculus RFFYTYIPFYGILGALVFEINFIREFLESHWFWVTQMNHLVMEIDLH---YRDWFSQOLA  
 242 T.thermophila N-----QN--FYIVLSELJAGFFSASLLVGNHENEMKFERR--ITLPEFEHOIA

375 M.alpina TGRDVH-PGLFANWFTCGGLNYQIEHHLLFPSMPRHNFSKIQPAVETLCKKYNMRYHTTGM  
 371 C.elegans TIRNMR-PGREIDWLWGGLNYQIEHHLLFPTMPRHNLTNTPLVKEFAAANGLPYMWDDYF  
 353 B.officinalis GTLDIS-CPPWMDWFHGGLOFQIEHHLLFPKMPRCNLRKISPYVIELCKKHNLPYNYASF  
 362 M.musculus ATCNVE-QSFENDWFSGHLNFOIEHHLLFPTMPRHNLHKIAPLVKSLCAKHGLEEQEKPILL  
 288 T.thermophila ASRNYAFHDIIESLLIMGGMQYQTEHHFFFPQIPPFYRLPKARVLIAREELKKWNLIKHEGPTE

# Replacement Sheet

Figure 4C

M.alpina	434	EGTAEVFSRLNEVSKAASKMGKAQ-----	457
C.elegans	430	TGFWLEIEQFRNTANVAAKITKKIA-----	454
B.officinalis	412	KANEMTLRLRNTALQARDHTTKPLPKNLVWEALHTHG	448
M.musculus	421	RALIDIVSSLKKSCELWLDAYLHK-----	444
T.thermophila	348	EKSHI-----	352

Stucture of delta-6-Desaturase Gene

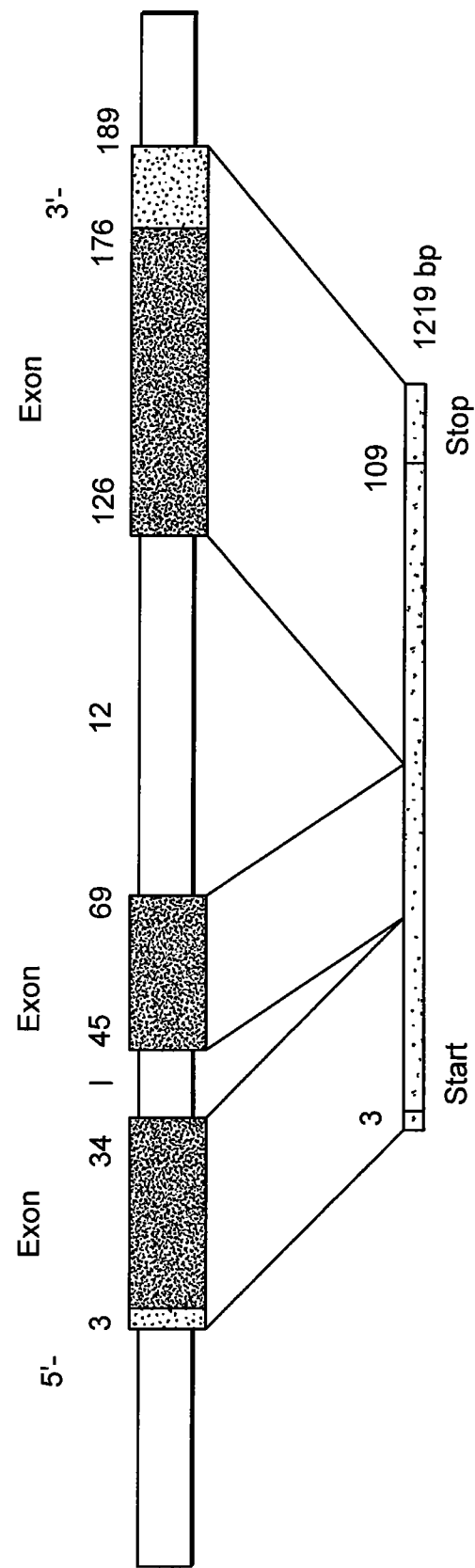


Figure 5

# Construction of pBDES6 Expressionconstruct

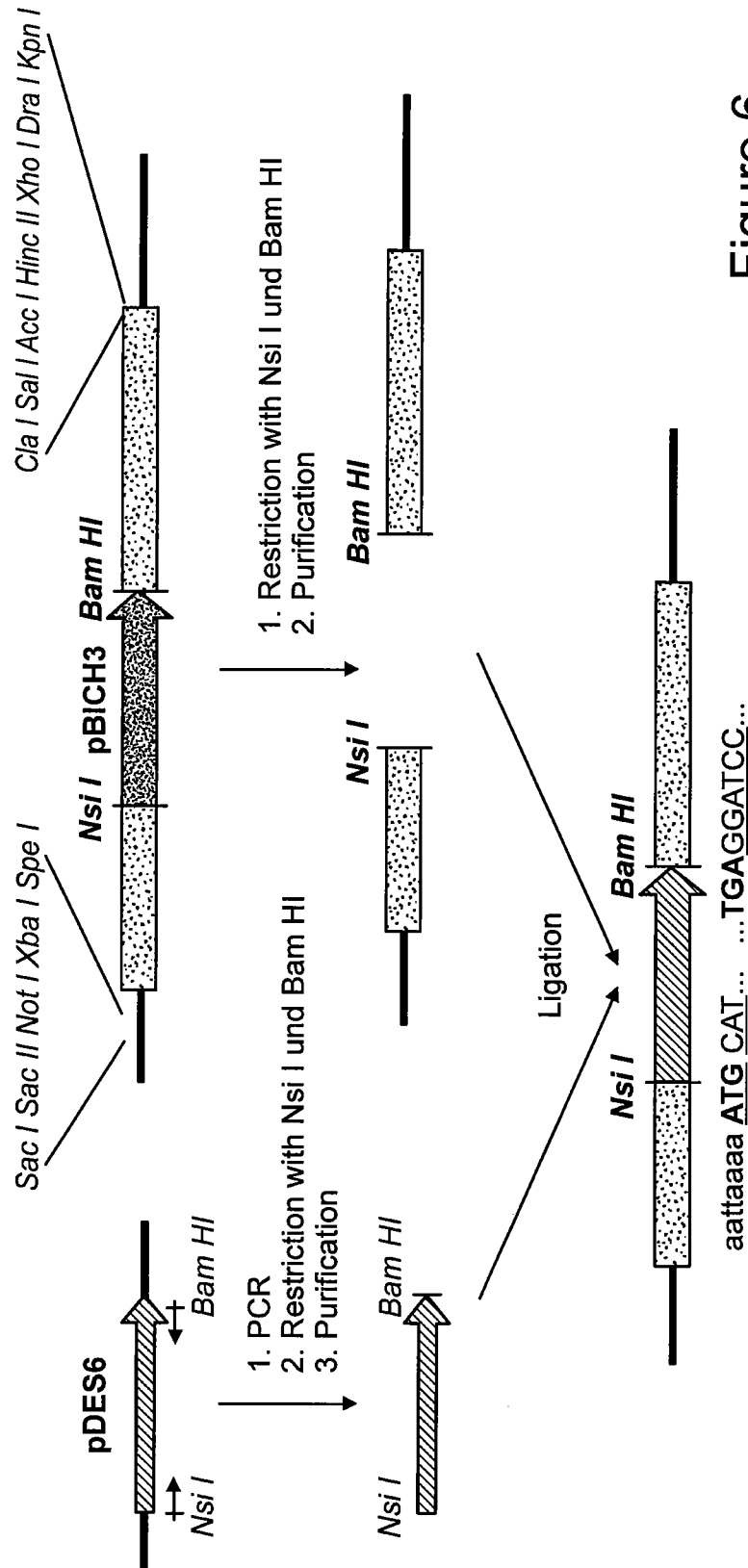
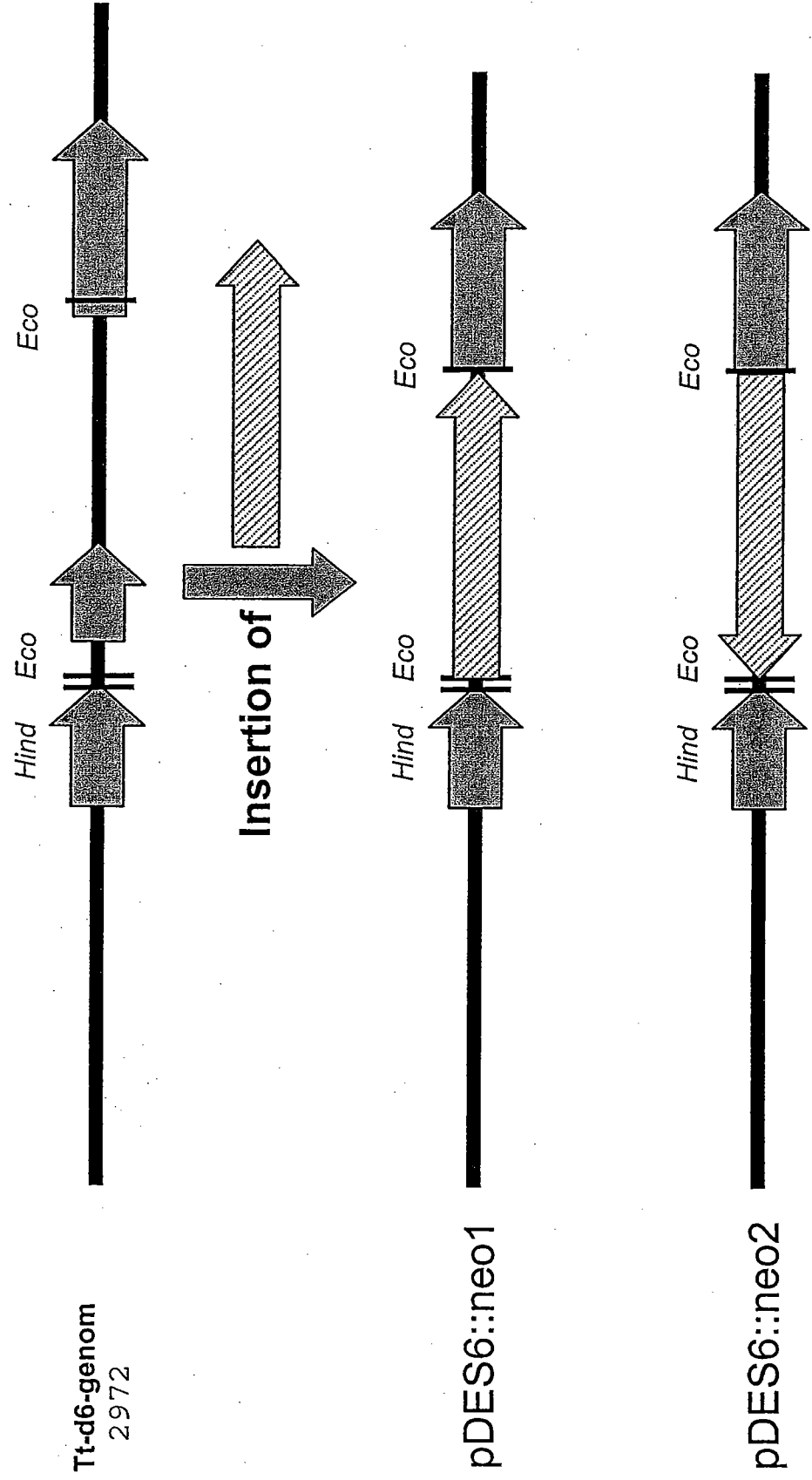
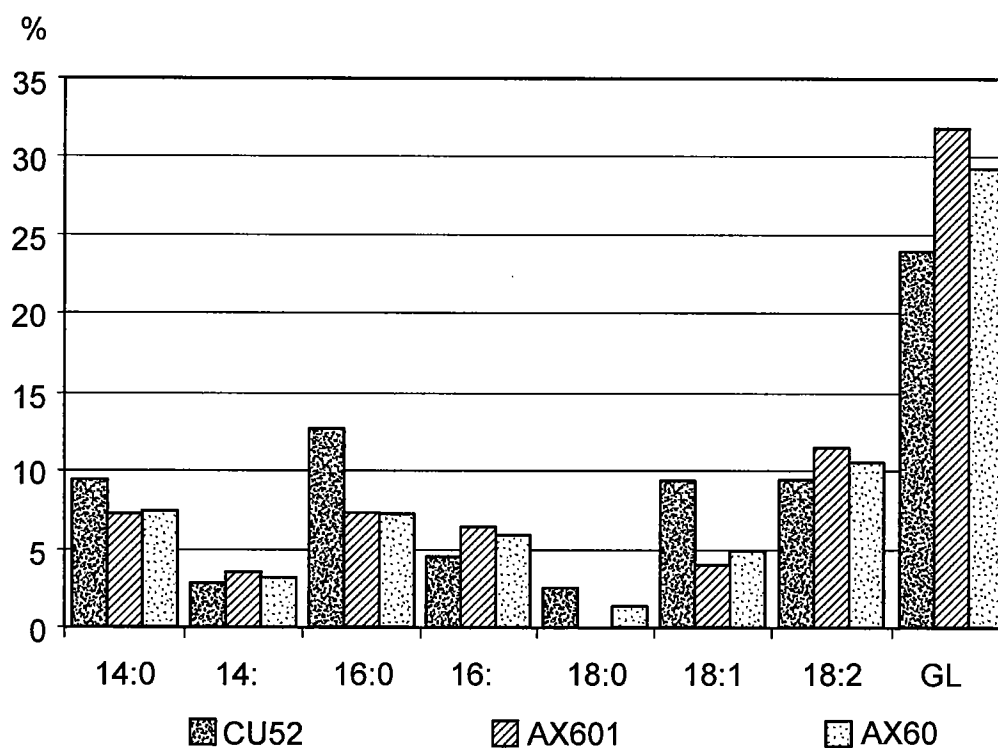


Figure 6

pBDes6 delta-6 Desaturase Expressionconstruct

Figure 7





Comparison of the fatty acid spectrum (main fatty acids) of the *Tetrahymena* pBDES6-Transformants (AX601 and AX604) with *Tetrahymena* wild strain (CU522) after 50 h of cultivation. Value is the percentage of fatty acids relative to total fatty acids.

Figure 8